

L Number	Hits	Search Text	DB	Time stamp
5	31	schmitz-gerd.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:12
6	0	klucken-jochen.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:12
7	475	atp same binding same cassette	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:13
8	267	atp same binding same cassette same gene	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:24
9	59	abca1	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:24

Sequence Comparison A

RESULT 2

ABC1_MOUSE

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ID  ABC1_MOUSE      STANDARD;      PRT;  2261 AA.
AC  P41233;
DT  01-FEB-1995 (Rel. 31, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE  transporter 1) (ATP-binding cassette 1) (ABC-1).
GN  ABCA1 OR ABC1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DBA/2; TISSUE=Macrophage;
RX  MEDLINE=94375008; PubMed=8088782;
RA  Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT  "Cloning of two novel ABC transporters mapping on human chromosome
RT  9.";
RL  Genomics 21:150-159(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=21251004; PubMed=11352567;
RA  Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT  "Human and mouse ABCA1 comparative sequencing and transgenesis
RT  studies revealing novel regulatory sequences.";
RL  Genomics 73:66-76(2001).
CC  -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC  TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC  TRANSPORT (BY SIMILARITY).
CC  -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC  LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC  -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC  EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC  ATP BINDING CASSETTE (ABC) DOMAIN.
CC  -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
CC  similarity).
CC  -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  -----
DR  EMBL; X75926; CAA53530.1; ALT_INIT.
DR  EMBL; AF287263; AAG39073.1; ALT_INIT.
DR  MGD; MGI:99607; Abcal.
DR  GO; GO:0008203; P:cholesterol metabolism; IDA.
DR  GO; GO:0030301; P:cholesterol transport; IDA.
DR  InterPro; IPR003593; AAA_ATPase.
DR  InterPro; IPR003439; ABC_transporter.
DR  Pfam; PF00005; ABC_tran; 2.
DR  ProDom; PD000006; ABC_transporter; 2.
DR  SMART; SM00382; AAA; 2.
DR  PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR  PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW  ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.
FT  TRANSMEM      26      42      POTENTIAL.
FT  TRANSMEM     640     656      POTENTIAL.
FT  TRANSMEM     690     706      POTENTIAL.
FT  TRANSMEM     717     733      POTENTIAL.
FT  TRANSMEM     749     765      POTENTIAL.

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FT	TRANSMEM	771	787	POTENTIAL.
FT	TRANSMEM	1041	1057	POTENTIAL.
FT	TRANSMEM	1351	1367	POTENTIAL.
FT	TRANSMEM	1661	1677	POTENTIAL.
FT	TRANSMEM	1708	1724	POTENTIAL.
FT	TRANSMEM	1737	1753	POTENTIAL.
FT	TRANSMEM	1775	1791	POTENTIAL.
FT	TRANSMEM	1854	1870	POTENTIAL.
FT	NP_BIND	933	940	ATP (POTENTIAL).
FT	NP_BIND	1946	1953	ATP (POTENTIAL).
FT	MOD_RES	1042	1042	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	MOD_RES	2054	2054	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	820	820	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1144	1144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1294	1294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1453	1453	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1499	1499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1504	1504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1637	1637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2238	2238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1567	1568	MISSING (IN REF. 2).
FT	CONFLICT	2024	2024	MISSING (IN REF. 2).
SQ	SEQUENCE	2261	AA; 254011	MW; FAE62B21FD1D09F9 CRC64;

Query Match 95.1%; Score 10906; DB 1; Length 2261;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVGQIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT	60
Db	61	MPSAGTLPWVGQIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQKDT	120
Qy	61	SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH	120
Db	121	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ	180
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELGCLPREKLAAAERVLRNMDILKPIL	180
Db	181	KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRNMDILKPVV	240
Qy	181	RTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRSWSDMRQEVFMFLTNVNSSSSSTQI	240
Db	241	TKLNSTSHLPTQHLEATTVLLDSLGLAQELFSTKSWSMDMRQEVFMFLTNVNSSSSSTQI	300
Qy	241	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK	300
Db	301	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK	360
Qy	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	360
Db	361	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	420
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTQAQDIVAFLAKHPEDVQSSNGS	420
Db	421	PQIWTFMENSQEMDLVRLTLLDSRGNDQFWEQKLDGLDWTQAQDIMAFLAKNPEDVQSPNGS	480

Qy 421 VYTWREAFNETNQAI RTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
 Db 481 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTVRLINKSMELLDERKFWAGIVFTG 540
 Qy 481 ITPGSIELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
 Db 541 ITPDSVELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 600
 Qy 541 EQAIIRVLTGTTEKKTGVYMQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKIGIV 600
 Db 601 EQAIIRVLTGTSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKSIV 660
 Qy 601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVILKLGNNLLPYSDPSVVFV 660
 Db 661 YEKEARLKETMRIMGLDNGILWFSWVFSSLIPLLVSAGLLVILKLGNNLLPYSDPSVVFV 720
 Qy 661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
 Db 721 FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFSIKIFAS 780
 Qy 721 LLSPVAFGFGCEYFALFEEQIGIGVQWDLNLFESPVVEEDGFNLTTSVSMMLFDFTLYGVMTW 780
 Db 781 LLSPVAFGFGCEYFALFEEQIGIGVQWDLNLFESPVVEEDGFNLTTAVSMMLFDFTLYGVMTW 840
 Qy 781 YIEAVFPGQYGI PRPWYFPCTKSYWFGESDEKSHPGSNQKRISEICMEEEPHKLKLGVS 840
 Db 841 YIEAVFPGQYGI PRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHKLRLGVS 900
 Qy 841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
 Db 901 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960
 Qy 901 GKDIRSEMSTIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 960
 Db 961 GKDIRSEMSSIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 1020
 Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
 Db 1021 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1080
 Qy 1021 GRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESLS 1080
 Db 1081 GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESLS 1140
 Qy 1081 SCRNSSTVSYLKKEDSVSQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
 Db 1141 SCRNSSTVSCLKKEDSVSQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1200
 Qy 1141 GHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEEIFLKVAEESGVDAE 1200
 Db 1201 GHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEEIFLKVAEESGVDAE 1260
 Qy 1201 TSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK 1260
 Db 1261 TSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETDLGMDGKGSYQLK 1320
 Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
 Db 1321 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1380
 Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEWTAP 1380
 Db 1381 PWMYNEQYTFVSNDAPEDMGTQELLNALTDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440
 Qy 1381 VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
 Db 1441 VPQSIVDLFQNGNWTMTKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQNL 1500
 Qy 1441 TGRNISDYLKTYVQIIAKSLKNKIWNENFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500

Db 1501 TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560
 Qy 1501 HLKLAkdSSADrFLNSlGRfMTGLDTRnnVkvWFnnKGWHAiSSfLNvINNAILrANLQK 1560
 Db 1561 LLKLTkDTSADrFLSSlGRfMAGLDtKNNVkvWFnnKGWHAiSSfLNvINNAILrANLQK 1620
 Qy 1561 GENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVVFLIQR 1620
 Db 1621 GENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQR 1680
 Qy 1621 VSKAKHLQFISGVKPVYWLNSFVWDMCNYVVPATLVIIIFICFQKSYVSSTNLPVLAL 1680
 Db 1681 VSKAKHLQFISGVKPVYWLNSFVWDMCNYVVPATLVIIIFICFQKSYVSSTNLPVLAL 1740
 Qy 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN 1740
 Db 1741 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1800
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920
 Qy 1861 YRRKRKPAVDRCVGIPPGECFGLLGvNgAGKSSTfKMLTGDTTVTRGDAFLNRNSILSN 1920
 Db 1921 YRRKRKPAVDRCIGIPPGECFGLLGvNgAGKSTTFKMLTGDPVTRGDAFLNKNSILSN 1980
 Qy 1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGEWAIrKLGLVKYGEK 1980
 Db 1981 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIrKLGLVKYGEK 2040
 Qy 1981 YAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
 Db 2041 YAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSIvKEGRSVVLT 2100
 Qy 2041 SHSMEECEALCTrMAIMVNGrFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDlKPvQDFFG 2100
 Db 2101 SHSMEECEALCTrMAIMVNGrFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDlKPvQEFFG 2160
 Qy 2101 LAFPGSVpKEKhrNMLQYQLPSSLSLARIFSILSQSKRLHIEdYSVSQTlDQVfVNF 2160
 Db 2161 LAFPGSVLKEKhrNMLQYQLPSSLSLARIFSILSQSKRLHIEdYSVSQTlDQVfVNF 2220
 Qy 2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSfLQDEKVKESYV 2201
 Db 2221 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSfLQDEKVKESYV 2261

Sequence Comparison B

RESULT 1

ABCI_HUMAN

ID ABC1_HUMAN STANDARD; PRT; 2261 AA.
AC O95477; Q96S56; Q96T85; Q9NQV4; Q9UN06; Q9UN07; Q9UN08; Q9UN09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux
DE regulatory protein).
GN ABCA1 OR ABC1 OR CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345099; PubMed=10884428;
RA Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA Haudenschild C.C., Prades C., Chimini G., Blackmon E.E.,
RA Francois T.L., Duverger N., Rubin E.M., Rosier M., Deneffe P.,
RA Fredrickson D.S., Brewer H.B. Jr.;
RT "Complete genomic sequence of the human ABCA1 gene: analysis of the
RT human and mouse ATP-binding cassette A promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Schwartz K., Lawn R.M., Wade D.P.;
RT "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
RT regulated by LXR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21251004; PubMed=11352567;
RA Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and transgenesis
RT studies revealing novel regulatory sequences.";
RL Genomics 73:66-76(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,
RA Kioka N., Amachi T., Yokoyama S., Ueda K.;
RT "A new topological model of functional human ABCA1-signal peptide
RT cleavage and glycosylation of a large extracellular domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE=99194549; PubMed=10092505;
RA Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,
RA Chimini G., Kaminski W.E., Schmitz G.;
RT "Molecular cloning of the human ATP-binding cassette transporter 1
RT (hABCA1): evidence for sterol-dependent regulation in macrophages.";
RL Biochem. Biophys. Res. Commun. 257:29-33(1999).
RN [6]
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE=99364413; PubMed=10431238;
RA Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
RA Deleuze J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
RT "Tangier disease is caused by mutations in the gene encoding
RT ATP-binding cassette transporter 1.";
RL Nat. Genet. 22:352-355(1999).
RN [7]
RP PHOSPHORYLATION OF SER-1042 AND SER-2054.
RX MEDLINE=22289331; PubMed=12196520;
RA See R.H., Caday-Malcolm R.A., Singaraja R.R., Zhou S., Silverston A.,
RA Huber M.T., Moran J., James E.R., Janoo R., Savill J.M., Rigot V.,

RA Zhang L.H., Wang M., Chimini G., Wellington C.L., Tafuri S.R.,
 RA Hayden M.R.;
 RT "Protein kinase A site-specific phosphorylation regulates ATP-binding
 RT cassette A1 (ABCA1)-mediated phospholipid efflux.";
 RL J. Biol. Chem. 277:41835-41842(2002).
 RN [8]
 RP VARIANTS HDLD2 THR-1091 AND 1893-GLU-ASP-1894 DEL.
 RX MEDLINE=20001430; PubMed=10533863;
 RA Marcil M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
 RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,
 RA Ouelette B.F.F., Sensen C.W., Fichter K., Mott S., Denis M.,
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective
 RT cholesterol efflux.";
 RL Lancet 354:1341-1346(1999).
 RN [9]
 RP VARIANTS HDLD1 ARG-597 AND ARG-1477, AND VARIANT HDLD2 LEU-693 DEL.
 RX MEDLINE=99364411; PubMed=10431236;
 RA Brooks-Wilson A., Marcil M., Clee S.M., Zhang L.-H., Roomp K.,
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
 RA Loubser O., Ouelette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
 RA Sensen C.W., Scherer S., Mott S., Denis M., Martindale D.,
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Mutations in ABC1 in Tangier disease and familial high-density
 RT lipoprotein deficiency.";
 RL Nat. Genet. 22:336-345(1999).
 RN [10]
 RP VARIANTS HDLD1 SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
 RP MET-883.
 RX MEDLINE=99364412; PubMed=10431237;
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
 RA Diederich W., Drobnik W., Barlage S., Buechler C.,
 RA Porsch-Oezcuemez M., Kaminski W.E., Hahmann H.W., Oette K.,
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
 RT Tangier disease.";
 RL Nat. Genet. 22:347-351(1999).
 RN [11]
 RP VARIANTS HDLD1 ILE-929; ARG-597 AND ARG-1477, AND VARIANTS HDLD2
 RP LEU-693 DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
 RX MEDLINE=20540002; PubMed=11086027;
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marcil M., Roomp K.,
 RA Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stulc T.,
 RA Suda T., Ceska R., Boucher B., Rondeau C., DeSouich C.,
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
 RA Hayden M.R.;
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
 RT coronary artery disease in ABCA1 heterozygotes.";
 RL J. Clin. Invest. 106:1263-1270(2000).
 RN [12]
 RP VARIANTS HDLD1 ASN-1289 AND HIS-1800.
 RX MEDLINE=20171564; PubMed=10706591;
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
 RA Van Eerdewegh P., Goldkamp A.L., Thurston L.M., FitzGerald M.G.,
 RA Yasek-McKenna D., O'Neill G., Eberhart G.P., Weiffenbach B.,
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
 RT tangier disease kindreds.";
 RL J. Lipid Res. 41:433-441(2000).
 RN [13]
 RP VARIANT HDLD1 ASP-1046, VARIANT HDLD2 CYS-230, AND VARIANTS LYS-219;
 RP ILE-825; MET-883 AND LYS-1587.
 RX MEDLINE=20396633; PubMed=10938021;
 RA Wang J., Burnett J.R., Near S., Young K., Zinman B., Hanley A.J.G.,
 RA Connelly P.W., Harris S.B., Hegele R.A.;
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
 RN [14]
 RP VARIANT HDLD1 TRP-587, AND VARIANT LEU-2168.
 RX MEDLINE=21157002; PubMed=11257260;

RA Bertolini S., Pisciotto L., Seri M., Cusano R., Cantafora A.,
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
 RT "A point mutation in ABC1 gene in a patient with severe premature
 RT coronary heart disease and mild clinical phenotype of Tangier
 RT disease.";
 RL Atherosclerosis 154:599-605(2001).
 RN [15]
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.
 RX MEDLINE=21157003; PubMed=11257261;
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kielar D.,
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
 RA Schmitz G.;
 RT "Common variants in the gene encoding ATP-binding cassette transporter
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.";
 RL Atherosclerosis 154:607-611(2001).
 RN [16]
 RP VARIANT HDLD1 LEU-1506.
 RX MEDLINE=21369429; PubMed=11476961;
 RA Lapicka-Bodzioch K., Bodzioch M., Kruell M., Kielar D., Probst M.,
 RA Klec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
 RA Suttorp N., Schmitz G.;
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of
 RT the ABCA1 gene and its application in genetic analysis of a new
 RT patient with familial high-density lipoprotein deficiency syndrome.";
 RL Biochim. Biophys. Acta 1537:42-48(2001).
 RN [17]
 RP VARIANTS HDLD1 ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
 RX MEDLINE=21369433; PubMed=11476965;
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier
 RT disease and familial high density lipoprotein deficiency with
 RT coronary heart disease.";
 RL Biochim. Biophys. Acta 1537:71-78(2001).
 RN [18]
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.
 RX MEDLINE=21138379; PubMed=11238261;
 RA Clee S.M., Zwiderman A.H., Engert J.C., Zwarts K.Y.,
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Wijland M., van Dam M.,
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Common genetic variation in ABCA1 is associated with altered
 RT lipoprotein levels and a modified risk for coronary artery disease.";
 RL Circulation 103:1198-1205(2001).
 RN [19]
 RP VARIANT HDLD1 THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.
 RX MEDLINE=21645894; PubMed=11785958;
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,
 RA Ishihara M., Sakane N., Zhang Z., Tsujii K., Matsuyama A., Ohama T.,
 RA Matsuura F., Ishigami M., Sakai N., Hiraoka H., Hattori H.,
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,
 RA Yamashita S., Matsuzawa Y.;
 RT "Expression and functional analyses of novel mutations of ATP-binding
 RT cassette transporter-1 in Japanese patients with high-density
 RT lipoprotein deficiency.";
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).
 CC -!- FUNCTION: cAMP-dependent and sulfonylurea-sensitive anion
 CC transporter. Key gatekeeper influencing intracellular cholesterol
 CC transport.
 CC -!- TISSUE SPECIFICITY: Widely expressed, but most abundant in
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Db	841	YIEAVFPGQYGIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISICMEEEPHTHLKLGVS	900
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Qy	901	GKDIRSEMSTIRQNLGVCQHNVLFDMLTVEEHIWFYARLKGKLGSEKHVKAEMEOMALDVG	960
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Qy	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ	1020
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09786635 Results

SEQ ID NO: 1

SUMMARIES

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AF165281

LOCUS AF165281 9497 bp mRNA linear PRI 17-AUG-1999

DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.

ACCESSION AF165281

VERSION AF165281.1 GI:5734100

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 9497)

AUTHORS Rust, S., Rosier, M., Funke, H., Real, J., Amoura, Z., Piette, J.C., Deleuze, J.F., Brewer, H.B., Duverger, N., Deneffe, P. and Assmann, G.

TITLE Tangier disease is caused by mutations in the gene encoding

ATP-binding cassette transporter 1

JOURNAL Nat. Genet. 22 (4), 352-355 (1999)

MEDLINE 99364413

PUBMED 10431238

REFERENCE 2 (bases 1 to 9497)

AUTHORS Rust, S., Rosier, M., Funke, H., Real, J., Amoura, Z., Piette, J.C., Deleuze, J.F., Brewer, H.B., Duverger, N., Deneffe, P. and Assmann, G.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston Cr#mieux, Evry 91006, France

FEATURES Location/Qualifiers

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gene

CDS

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Qy	601		AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG	660
Db	601		AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG	660
Qy	661		AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Db	661		AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Qy	721		TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	780
Db	721		TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	780
Qy	781		ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Db	781		ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Qy	841		TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG	900
Db	841		TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG	900
Qy	901		TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Db	901		TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Qy	961		GAAGATGCTGAAACCTTCTATGACAACCTACAACCTCCTTACTGCAATGATTTGATGAAG	1020
Db	961		GAAGATGCTGAAACCTTCTATGACAACCTACAACCTCCTTACTGCAATGATTTGATGAAG	1020
Qy	1021		AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Db	1021		AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Qy	1081		GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Db	1081		GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Qy	1141		AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
Db	1141		AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
Qy	1201		CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG	1260
Db	1201		CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG	1260

Qy	1261	GACAGCAGGGACAATGACCACCTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1320
Db	1261	GACAGCAGGGACAATGACCACCTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1320
Qy	1321	CAAGACATCGTGGCGTTTTTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380
Db	1321	CAAGACATCGTGGCGTTTTTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380
Qy	1381	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGACCATATCTCGC	1440
Db	1381	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGACCATATCTCGC	1440
Qy	1441	TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCATAGCAACAGAAGTCTGGCTCATC	1500
Db	1441	TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCATAGCAACAGAAGTCTGGCTCATC	1500
Qy	1501	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA	1560
Db	1501	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA	1560
Qy	1561	ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1620
Db	1561	ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1620
Qy	1621	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCTTGGTCTCGAGCT	1680
Db	1621	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCTTGGTCTCGAGCT	1680
Qy	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740
Db	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740
Qy	1741	GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAAGTGGTGTCTATATGCAA	1800
Db	1741	GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAAGTGGTGTCTATATGCAA	1800
Qy	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG	1860
Db	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG	1860
Qy	1861	CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1920
Db	1861	CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1920
Qy	1921	TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC	1980
Db	1921	TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC	1980
Qy	1981	CTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTA	2040
Db	1981	CTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTA	2040
Qy	2041	GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTGTC	2100
Db	2041	GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTGTC	2100
Qy	2101	TTCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC	2160
Db	2101	TTCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC	2160
Qy	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
Db	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
Qy	2221	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280
Db	2221	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280
Qy	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGGCCCTTTTGTAGGAGCAG	2340
Db	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGGCCCTTTTGTAGGAGCAG	2340

Qy	2341	GGCATTGGAGTGCAGTGGGACAACTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT	2400
Db	2341	GGCATTGGAGTGCAGTGGGACAACTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT	2400
Qy	2401	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2460
Db	2401	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2460
Qy	2461	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCCCTGGTATTTTCCTTGC	2520
Db	2461	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCCCTGGTATTTTCCTTGC	2520
Qy	2521	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2580
Db	2521	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2580
Qy	2581	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2640
Db	2581	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2640
Qy	2641	ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCTGGCA	2700
Db	2641	ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCTGGCA	2700
Qy	2701	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	2760
Db	2701	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	2760
Qy	2761	ACCACCATGTCAATCCTGACCGGTTGTTCCTCCCGACCTCGGGCACCGCCTACATCCTG	2820
Db	2761	ACCACCATGTCAATCCTGACCGGTTGTTCCTCCCGACCTCGGGCACCGCCTACATCCTG	2820
Qy	2821	GGAAAAGACATTCTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG	2880
Db	2821	GGAAAAGACATTCTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG	2880
Qy	2881	CATAACGTGCTGTTTGACATGCTGACTGTCTGAAGAACACATCTGGTTCTATGCCCGCTTG	2940
Db	2881	CATAACGTGCTGTTTGACATGCTGACTGTCTGAAGAACACATCTGGTTCTATGCCCGCTTG	2940
Qy	2941	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3000
Db	2941	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3000
Qy	3001	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG	3060
Db	3001	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG	3060
Qy	3061	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCTATTCTGGATGAACCCACA	3120
Db	3061	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCTATTCTGGATGAACCCACA	3120
Qy	3121	GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3180
Db	3121	GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3180
Qy	3181	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240
Db	3181	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240
Qy	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Db	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Qy	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Db	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Qy	3361	TCCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGGACAGTGTTCCTCAG	3420

Db 3361 TCCTGCAGAAACAGTAGTAGCTGTGTACCTGAAAAAGGAGGACAGTGTTCCTCAG 3420
 Qy 3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
 |||||
 Db 3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
 Qy 3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGAAGACATA 3540
 |||||
 Db 3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGAAGACATA 3540
 Qy 3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
 |||||
 Db 3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
 Qy 3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA 3660
 |||||
 Db 3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA 3660
 Qy 3661 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
 |||||
 Db 3661 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
 Qy 3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
 |||||
 Db 3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
 Qy 3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCCA 3840
 |||||
 Db 3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCCA 3840
 Qy 3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA 3900
 |||||
 Db 3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA 3900
 Qy 3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
 |||||
 Db 3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
 Qy 3961 AGACGGAGTCGGAAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
 |||||
 Db 3961 AGACGGAGTCGGAAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
 Qy 4021 GCCCTTGTGTTTCAAGCTGATCGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACTTCAG 4080
 |||||
 Db 4021 GCCCTTGTGTTTCAAGCTGATCGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACTTCAG 4080
 Qy 4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
 |||||
 Db 4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
 Qy 4141 ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
 |||||
 Db 4141 ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
 Qy 4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
 |||||
 Db 4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
 Qy 4261 GTTCCCCAGACCATCATGGACCTCTTCAGAAATGGGAACTGGACAATGCAGAACCCCTTCA 4320
 |||||
 Db 4261 GTTCCCCAGACCATCATGGACCTCTTCAGAAATGGGAACTGGACAATGCAGAACCCCTTCA 4320
 Qy 4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG 4380
 |||||
 Db 4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG 4380
 Qy 4381 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
 |||||
 Db 4381 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
 Qy 4441 ACAGGAAGAAACATTTTCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500

Db	4441		ACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4500
Qy	4501		TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCTGGGTGTCACT	4560
Db	4501		TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCTGGGTGTCACT	4560
Qy	4561		AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620
Db	4561		AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620
Qy	4621		CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4680
Db	4621		CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4680
Qy	4681		ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740
Db	4681		ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740
Qy	4741		GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCGGGCCAACCTGCAAAAG	4800
Db	4741		GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCGGGCCAACCTGCAAAAG	4800
Qy	4801		GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAG	4860
Db	4801		GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAG	4860
Qy	4861		CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTGTGTCCATCTGT	4920
Db	4861		CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTGTGTCCATCTGT	4920
Qy	4921		GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCTGATTCTGATCCAGGAGCGG	4980
Db	4921		GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCTGATTCTGATCCAGGAGCGG	4980
Qy	4981		GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040
Db	4981		GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040
Qy	5041		TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
Db	5041		TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
Qy	5101		TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT	5160
Db	5101		TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT	5160
Qy	5161		CTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220
Db	5161		CTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220
Qy	5221		AAGATCCCCAGCACAGCCTATGTGGTGCTACCAGCGTGAACCTCTTCATTGGCATTAAAT	5280
Db	5221		AAGATCCCCAGCACAGCCTATGTGGTGCTACCAGCGTGAACCTCTTCATTGGCATTAAAT	5280
Qy	5281		GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340
Db	5281		GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340
Qy	5341		GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTTCCTGGGACGAGGGCTCATC	5400
Db	5341		GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTTCCTGGGACGAGGGCTCATC	5400
Qy	5401		GACATGGTGAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460
Db	5401		GACATGGTGAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460
Qy	5461		GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520
Db	5461		GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520

Qy	5521	GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT	5580
Db	5521	GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT	5580
Qy	5581	GTAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG	5640
Db	5581	GTAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG	5640
Qy	5641	AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	5700
Db	5641	AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	5700
Qy	5701	TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCTGGTGAG	5760
Db	5701	TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCTGGTGAG	5760
Qy	5761	TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA	5820
Db	5761	TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA	5820
Qy	5821	GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC	5880
Db	5821	GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC	5880
Qy	5881	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	5940
Db	5881	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	5940
Qy	5941	TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6000
Db	5941	TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6000
Qy	6001	GTTGGCAAGGTTGGTGAAGTGGGCGATTTCGGAACCTGGGCCTCGTGAAGTATGGAGAAAA	6060
Db	6001	GTTGGCAAGGTTGGTGAAGTGGGCGATTTCGGAACCTGGGCCTCGTGAAGTATGGAGAAAA	6060
Qy	6061	TATGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6120
Db	6061	TATGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6120
Qy	6121	GGCGGGCCTCCTGTGGTGTCTTGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG	6180
Db	6121	GGCGGGCCTCCTGTGGTGTCTTGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG	6180
Qy	6181	CGGTTCTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACA	6240
Db	6181	CGGTTCTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACA	6240
Qy	6241	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6300
Db	6241	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6300
Qy	6301	AGGTTCCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAATAGGTTTGAGATGGTTATACA	6360
Db	6301	AGGTTCCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAATAGGTTTGAGATGGTTATACA	6360
Qy	6361	ATAGTTGTACGAATAGCAGGTCACCCGACCTGAAGCCTGTCCAGGATTCTTTGGA	6420
Db	6361	ATAGTTGTACGAATAGCAGGTCACCCGACCTGAAGCCTGTCCAGGATTCTTTGGA	6420
Qy	6421	CTTGCAATTCCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT	6480
Db	6421	CTTGCAATTCCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT	6480
Qy	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTGAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Db	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTGAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Qy	6541	CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT	6600
Db	6541	CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT	6600

Qy 6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660
 ||||||||||||||||||
 Db 6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660
 Qy 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 ||||||||||||||||||
 Db 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 Qy 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT 6780
 ||||||||||||||||||
 Db 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGNACTAGACTTTCCTTT 6780
 Qy 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 ||||||||||||||||||
 Db 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 Qy 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880
 ||||||||||||||||||
 Db 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6880	100.0	6880	21	AAZ94734	Human ATP binding
2	6880	100.0	6880	22	AAI70314	Human ATP binding
3	6880	100.0	7260	22	AAD21326	Human ATP binding
4	6880	100.0	7260	22	AAI70315	Human ATP binding
5	6879	100.0	9497	24	ABV78020	Hypoxia-regulated
6	6876.8	100.0	6880	22	AAD21325	Human ATP binding
7	6875.8	99.9	9741	22	AAS06120	Human ABC1 DNA seq
8	6875.8	99.9	9741	24	AAD37273	Human ABC1 full-le
9	6875.8	99.9	9854	22	AAS06121	Human ABC1 DNA seq
10	6875.8	99.9	9870	24	ABN99301	Polymorphic human
11	6875.8	99.9	9870	24	ABN99302	Polymorphic human
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Polymorphic human

SUMMARIES

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	Score	Match	Length			
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4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap
c 9	83.8	1.2	2253	4	US-09-252-991A-3810	Sequence 3810, Ap
10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
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SUMMARIES

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5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GI0-
c 6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-
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RESULT 1

AK051920

LOCUS AK051920 4783 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
enriched library, clone:D230019D04 product:ATP-binding cassette,
sub-family A (ABC1), member 1, full insert sequence.

ACCESSION AK051920

VERSION AK051920.1 GI:26342297

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
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AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

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AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 12085660

REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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BASE COUNT 1119 a 1236 c 1310 g 1118 t

ORIGIN

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Matches 3901; Conservative 0; Mismatches 501; Indels 0; Gaps 0;

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Db	2362	CTCTGGTTTAGCTGGTTTGTTAGCAGCCTCATCCCTCTGCTTGTGAGCGCTGGCCTGCTG	2421
Qy	2041	GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC	2100
Db	2422	GTGGTCATCTTGAAGTTAGGAAACCTGCTGCCCTATAGTGACCCACGCGTGGTGTTGTC	2481
Qy	2101	TTCTGTGCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTTC	2160
Db	2482	TTCTGTCTGTGTTTGGCCATGGTGACCATCTACAGTGCTTCTCTATTAGCAGCTCTTC	2541

Qy	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
Db	2542		
Qy	2221	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280
Db	2602		
Qy	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTTGCCCTTTTTCGAGGAGCAG	2340
Db	2662		
Qy	2341	GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2400
Db	2722		
Qy	2401	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2460
Db	2782		
Qy	2461	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCACAGGCCCTGGTATTTTCCTTGC	2520
Db	2842		
Qy	2521	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2580
Db	2902		
Qy	2581	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2640
Db	2962		
Qy	2641	ATTCAGAACCTGGTAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCTGATGGCCTGGCA	2700
Db	3022		
Qy	2701	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	2760
Db	3082		
Qy	2761	ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCACCGCCTACATCCTG	2820
Db	3142		
Qy	2821	GGAAAAGACATTCTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCAG	2880
Db	3202		
Qy	2881	CATAACGTGCTGTTTGACATGCTGACTGTGCGAAGAACACATCTGGTTCTATGCCCGCTTG	2940
Db	3262		
Qy	2941	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3000
Db	3322		
Qy	3001	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG	3060
Db	3382		
Qy	3061	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA	3120
Db	3442		
Qy	3121	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3180
Db	3502		
Qy	3181	GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240

Db	3562	GGCCGCACCATTATTTTGTCTACACACCACATGGACGAAGCTGACATCCTTGGGGACAGA	3621
Qy	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Db	3622	ATTGCCATCATTTCATGGGAAGCTGTGTTGTGTGGGCTCCTCCCTGTTTTTGAAAAAC	3681
Qy	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Db	3682	CAGTTGGGAACGGGTACTATCTGACCTTGGTAAAGAAAGATGTGGAATCGTCCCTCAGT	3741
Qy	3361	TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCCTCAG	3420
Db	3742	TCCTGCAGAAACAGTAGCAGCACCGTGTCTTGTCTGAAAAAGGAGGACAGTGTTCCTCAG	3801
Qy	3421	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC	3480
Db	3802	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAAAGTGACACGCTGACCATCGATGTC	3861
Qy	3481	TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAAGACATA	3540
Db	3862	TCTGCTATCTCCAACCTCATCAGGAAGCACGTGTCTGAAGCCCGGCTGGTGGAAGACATT	3921
Qy	3541	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTGTGGAA	3600
Db	3922	GGGCACGAGCTGACCTATGTGCTGCCGTACGAAGCCGCGAAGGAGGGAGCCTTGTGGAA	3981
Qy	3601	CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA	3660
Db	3982	CTCTTCCATGAGATTGATGACCGGCTCTCAGACCTGGGCATCTCCAGTTATGGCATCTCG	4041
Qy	3661	GAGACGACCCTGGAAGAAATATTCTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3720
Db	4042	GAGACCACCCTGGAAGAAATATTCTCTCAAGTGGCTGAAGAGAGCGGGGTGGATGCTGAG	4101
Qy	3721	ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGCCCTTCGGGGACAAGCAGAGC	3780
Db	4102	ACCTCAGATGGTACTTTGCCAGCAAGACGAAACAGACGCGGCCCTTCGGGGACAAGCAGAGC	4161
Qy	3781	TGTCTTCGCCCCCTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCCA	3840
Db	4162	TGTCTGCACCCATTTACGGAAGATGATGCTGTTGATCCCAATGACTCTGACATAGACCCA	4221
Qy	3841	GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA	3900
Db	4222	GAATCCAGGGAGACCGACCTGCTCAGTGGGATGGACGGCAAAGGGTCTACCAGCTGAAG	4281
Qy	3901	GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC	3960
Db	4282	GGCTGGAAACTCACCCAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGGCTGCTGATTGCC	4341
Qy	3961	AGACGGAGTCGGAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT	4020
Db	4342	AGACGGAGCCGGAAGGTTTCTTTGTCTCAGATTGTCTTGCCAGCTGTCTTTGTTTGATT	4401
Qy	4021	GCCCTTGTGTTTCAAGCTGATCGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACCTCAG	4080
Db	4402	GCCCTTGTGTTTCAAGCTGATTGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACCTCAG	4461
Qy	4081	CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA	4140
Db	4462	CCCTGGATGTATAATGAGCAGTATACATTTGTGAGTAATGATGCTCCCGAGGACATGGGC	4521
Qy	4141	ACCCTGGAACCTCTTAAACGCCCTCACAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4200
Db	4522	ACCAGGAACCTCTGAATGCTCTGACCAAAGATCCAGGCTTTGGGACCCGCTGTATGGAA	4581
Qy	4201	GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA	4260
Db	4582	GGAAACCCAATCCCAGATACCCCTTGCTTGGCTGGGGAGGAGGACTGGACCATCAGCCCC	4641
Qy	4261	GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCCTTCA	4320

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Db      4642  GTCCCCCAGAGCATCGTGGACCTCTTCCAGAATGGAAACTGGACCATGAAGAACCCTCA 4701
Qy      4321  CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
Db      4702  CCTGCGTGCCAGTGTAGCAGTGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4761
Qy      4381  GCAGGGGGGCTGCCTCCTCCAC 4402
Db      4762  GCAGGGGGGCTGCCACCTCCTC 4783

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SEQ ID NO: 2

Result No.	Score	Query Match	Length	DB	ID	Description
1	11469	100.0	2201	21	AAV79380	Human ATP binding
2	11469	100.0	2201	22	AAE13021	Human ATP binding
3	11469	100.0	2201	22	AAM50227	Human ATP binding
4	11469	100.0	2201	23	ABP65164	Hypoxia-regulated
5	11469	100.0	2261	22	AAE13022	Human ATP binding
6	11469	100.0	2261	22	AAM50228	Human ATP binding
7	11469	100.0	2261	22	AAU02176	Human ABC1. Homo
8	11469	100.0	2261	22	AAU02177	Human ABC1 mutant
9	11469	100.0	2261	23	ABB83111	Human ABCA1 transp
10	11469	100.0	2261	23	ABP52092	Homo sapiens ABC t
11	11469	100.0	2261	23	AAE23000	Human ABC1 full-le
12	11468	100.0	2261	23	ABB83117	Polymorphic human
13	11468	100.0	2261	23	ABB83124	Polymorphic human
14	11466	100.0	2261	22	AAU02183	Human ABC1 mutant
15	11466	100.0	2261	22	AAU02188	Human ABC1 mutant
16	11466	100.0	2261	23	ABB83115	Polymorphic human
17	11466	100.0	2261	23	ABB83116	Polymorphic human
18	11466	100.0	2261	23	ABB83119	Polymorphic human
19	11466	100.0	2261	23	ABB83122	Polymorphic human
20	11466	100.0	2261	23	ABB83123	Polymorphic human
21	11465	100.0	2261	22	AAU02189	Human ABC1 mutant
22	11464	100.0	2261	23	ABB83121	Polymorphic human
23	11463	99.9	2261	22	AAU02181	Human ABC1 mutant
24	11462	99.9	2261	22	AAM78550	Human protein SEQ
25	11462	99.9	2263	22	ABB11956	Human ABCA1 homolo
26	11462	99.9	2263	22	AAM79534	Human protein SEQ
27	11461	99.9	2261	22	AAU02182	Human ABC1 mutant
28	11461	99.9	2261	22	AAU02186	Human ABC1 mutant
29	11459	99.9	2261	23	ABB83118	Polymorphic human
30	11458	99.9	2261	23	ABB83120	Polymorphic human
31	11440	99.7	2261	21	AAB38082	Human ABC1 cholest
32	11440	99.7	2261	22	AAB71749	Human ABC1 protein
33	11440	99.7	2261	24	ABU11899	Human ATP-binding
34	11439	99.7	2261	23	ABB81578	Human ABC-A-1-1 pr
35	11437	99.7	2261	21	AAB38109	Human ABC1 cholest
36	11437	99.7	2261	21	AAB38111	Human ABC1 cholest
37	11437	99.7	2261	21	AAB38114	Human ABC1 cholest
38	11437	99.7	2261	21	AAB38115	Human ABC1 cholest
39	11437	99.7	2261	21	AAB38117	Human ABC1 cholest

No.	Score	Match	Length	DB	ID	Description
1	6909	60.2	1375	3	US-08-665-259-26	Sequence 26, Appl
2	6909	60.2	1375	3	US-08-762-500-26	Sequence 26, Appl
3	3129.5	27.3	1457	3	US-08-665-259-27	Sequence 27, Appl
4	3129.5	27.3	1457	3	US-08-762-500-27	Sequence 27, Appl
5	2635.5	23.0	1684	3	US-08-665-259-25	Sequence 25, Appl
6	2635.5	23.0	1684	3	US-08-762-500-25	Sequence 25, Appl
7	2635.5	23.0	1704	3	US-08-762-500-75	Sequence 75, Appl

8	359	3.1	315	4	US-09-328-352-4388	Sequence 4388, Ap
9	354	3.1	332	4	US-09-107-532A-3752	Sequence 3752, Ap
10	352.5	3.1	335	4	US-09-252-991A-20837	Sequence 20837, A
11	352	3.1	322	4	US-09-107-532A-4662	Sequence 4662, Ap
12	346	3.0	589	4	US-09-328-352-7592	Sequence 7592, Ap
13	336.5	2.9	1280	2	US-08-583-276-19	Sequence 19, Appl
14	335.5	2.9	291	4	US-09-107-532A-4205	Sequence 4205, Ap
15	335.5	2.9	1280	4	US-09-767-594-2	Sequence 2, Appli
16	335.5	2.9	1280	6	5206352-4	Patent No. 5206352
17	333	2.9	1279	2	US-08-784-649A-2	Sequence 2, Appli
18	332	2.9	402	4	US-09-107-532A-5360	Sequence 5360, Ap
19	330.5	2.9	1280	2	US-08-752-447-2	Sequence 2, Appli

RESULT 1

US-08-665-259-26

; Sequence 26, Application US/08665259

; Patent No. 6028173

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,259

; FILING DATE: 17-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-665-259-26

Query Match 60.2%; Score 6909; DB 3; Length 1375;

Best Local Similarity 96.9%; Pred. No. 0;

Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

Qy 827 CMEEEPHTLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886
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Db 1 CMEEEPHTLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy 887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKLGLSEK 946
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Db 61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKGLSEK 120
 Qy 947 HVKAEMEOMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 1006
 Db 121 HVKAEMEOMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180
 Qy 1007 SRRGIWELLKRYQGRITILSTHHMDEADVLDRIAIISHGKLCCVGSSSLFLKNQLGTGY 1066
 Db 181 SRRGIWELLKRYQGRITILSTHHMDEADVLDRIAIISHGKLCCVGSSSLFLKNQLGTGY 240
 Qy 1067 YLTLVKKDVESLSSCRNSSSTVSYLKEDSVSQSSSDAGLGDHESDTLTIDVSAISNL 1126
 Db 241 YLTLVKKDVESLSSCRNSSSTVSCLKEDSVSQSSSDAGLGDHESDTLTIDVSAISNL 300
 Qy 1127 IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 1186
 Db 301 IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 360
 Qy 1187 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETD 1246
 Db 361 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSLHPFTEDDAVDPNDSIDPESRETD 420
 Qy 1247 LLSGMDGKGSYQVKGWKLTTQQQFVALLWKRLLIARRSRKGFQAQIVLPAVFCIALVFSL 1306
 Db 421 LLSGMDGKGSYQLKGWKLTTQQQFVALLWKRLLIARRSRKGFQAQIVLPAVFCIALVFSL 480
 Qy 1307 IVPFPGKYPSLELQPMWYNEQYTFVSNDAPEDTGTLELLNALT KD PFGTRCMEGNPIPD 1366
 Db 481 IVPFPGKYPSLELQPMWYNEQYTFVSNDAPEDMGTQELLNALT KD PFGTRCMEGNPIPD 540
 Qy 1367 TPCQAGEEWTTPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
 Db 541 TPCQAGEEDWTISPVQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600
 Qy 1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 1486
 Db 601 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 660
 Qy 1487 PSQEVNDATKQMKKHLKLAKDSSADRFNLNLTGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
 Db 661 PSHEVNDATKQMKKHLKLAKDSSADRFNLNLTGRFMTGLDTRNNVKVWFNNKGWHAISSFL 720
 Qy 1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 1606
 Db 721 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 780
 Qy 1607 FVPASFVFLIQUERVSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQQ 1666
 Db 781 FVPASFVFLIQUERVSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQQ 840
 Qy 1667 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
 Db 841 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900
 Qy 1727 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786
 Db 901 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960
 Qy 1787 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
 Db 961 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1020
 Qy 1847 GQNDILEIKELTKIYRRKRKPAVDRICGIPPGECFGLLVNGAGKSTTFKMLTGDTTPT 1906
 Db 1021 GQNDILEIKELTKIYRRKRKPAVDRICGIPPGECFGLLVNGAGKSTTFKMLTGDTTPT 1080
 Qy 1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVE 1966
 Db 1081 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVE 1140
 Qy 1967 WAIRKGLVKYGEKYAGNYSGGNKRKLSTAMALIGPPVFLDEPTTGMDPKARRFLWNC 2026

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Db      1141 WAIRKLGVLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC 1200
Qy      2027 ALSVVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086
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Db      1201 ALSIVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260
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Db      1261 GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSLARIFSILSQSKKRLHIEDY 1320
Qy      2147 SVSQTTLDQVFNFAKDQSDDDLKDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
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RESULT 2

US-08-762-500-26

; Sequence 26, Application US/08762500

; Patent No. 6030806

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/762,500

; FILING DATE: 09-DEC-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/665,259

; FILING DATE: 17-JUN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10469

; FILING DATE: 17-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-762-500-26

Query Match

60.2%; Score 6909; DB 3; Length 1375;


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Qy      1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE 1966
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Db      1081 RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFG 1140

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Db      1141 WAIRKGLLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC 1200

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Db      1201 ALSIVKEGRSVVLTSMSMEECEALCTRAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260

Qy      2087 GSNPDLKPVQDFGLAFPGSVPEKEHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDY 2146
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Db      1261 GSNPDLKPVQDFGLAFPGSVLKEKEHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDY 1320

Qy      2147 SVSQTTLDQVFNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
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Db      1321 SVSQTTLDQVFNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375

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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	10906	95.1	2201	2	A54774	ATP binding casset
2	3338.5	29.1	1529	2	A59189	ATP-binding casset
3	3129.5	27.3	1472	2	B54774	ATP binding casset
4	2638.5	23.0	1704	2	S71363	probable ATP-bindi
5	2635.5	23.0	1704	2	A59188	ATP-binding casset
6	2061	18.0	1802	2	T33783	hypothetical prote
7	1975	17.2	1816	2	A84845	probable ABC trans
8	1854.5	16.2	1447	2	T15200	hypothetical prote
9	1792	15.6	1317	2	C88925	protein F33E11.4 {
10	1535.5	13.4	1758	2	F88559	protein C48B4.4b {
11	1528.5	13.3	1704	2	T42749	ATP-binding casset
12	1526	13.3	1767	2	S60124	transport protein
13	1393	12.1	1246	2	T00826	hypothetical prote
14	1150.5	10.0	1564	2	T27121	hypothetical prote
15	1006.5	8.8	373	2	T47150	hypothetical prote
16	1005.5	8.8	1431	2	T22748	hypothetical prote
17	846	7.4	269	2	T46467	hypothetical prote
18	786.5	6.9	1011	2	T07712	probable ABC-type
19	695	6.1	900	2	T07717	probable ABC-type

RESULT 1

A54774

ATP binding cassette transporter ABC1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001

C;Accession: A54774

R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.

Genomics 21, 150-159, 1994

A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.

A;Reference number: A54774; MUID:94375008; PMID:8088782

A;Accession: A54774

A;Molecule type: mRNA

A;Residues: 1-2201 <LUC>

A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C;Keywords: ATP; duplication; nucleotide binding; P-loop

F;856-1047/Domain: ATP-binding cassette homology <ABC1>

F;873-880/Region: nucleotide-binding motif A (P-loop)

F;1869-2060/Domain: ATP-binding cassette homology <ABC2>
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 95.1%; Score 10906; DB 2; Length 2201;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

```
Qy      1 MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT 60
      |||
Db      1 MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQRDT 60

Qy     61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
      |||
Db     61 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLQXNVGLQ 120

Qy    121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKAAAERVLRSNMDILKPIL 180
      |||
Db    121 KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAERVLRYNMDILKPVV 180

Qy    181 RTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRWSDMRQEVMTNVSNSSSSTQI 240
      |||
Db    181 TKLNSTSHLPTQHLAEATTVLLDSLGLAQELFSTKWSDMRQEVMTNVSNSSSSTQI 240

Qy    241 YQAVSRIVCGHPEGGLKIKSLNWDYEDNNYKALFGGNGTEEDAETFDNSTTPYCNDLMK 300
      |||
Db    241 YQAVSRIVCGHPEGGLKIKSLNWDYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK 300

Qy    301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 360
      |||
Db    301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 360

Qy    361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTADQDIVAFLAKHPEDVQSSNGS 420
      |||
Db    361 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTADQDIMAFLAKNPEDVQSPNGS 420

Qy    421 VYTWREAFNETNQAIQTISRMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTG 480
      |||
Db    421 VYTWREAFNETNQAIQTISRMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTG 480

Qy    481 ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
      |||
Db    481 ITPDSVELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540

Qy    541 EQAIIRVLTGTEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIGIV 600
      |||
Db    541 EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIISIV 600

Qy    601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVILKGNLLPYSDPSVVFV 660
      |||
Db    601 YEKEARLKETMRIMGLDNGILWFSWVSSLIPLLVSAGLLVILKGNLLPYSDPSVVFV 660

Qy    661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSLKIFAS 720
      |||
Db    661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSLKIFAS 720

Qy    721 LLSPVAFGFGCEYFALFEEQGIGVQWDLNLFESPVEEDGFNLTTSVSMMLFDFTLYGVMTW 780
      |||
Db    721 LLSPVAFGFGCEYFALFEEQGIGVQWDLNLFESPVEEDGFNLTTAVSMMLFDFTLYGVMTW 780

Qy    781 YIEAVFPGQYGIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISICMEEEPTHLKLGVS 840
      |||
Db    781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPTHLRLGVS 840

Qy    841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
      |||
Db    841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900

Qy    901 GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGKLGSEKHVKAEMEQLMDVG 960
      |||
Db    901 GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGKLGSEKHVKAEMEQLMDVG 960
```

Qy	961	LPSSKLLSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSSRRGIWELLKRYQ	1020
Db	961	LPPSKLLSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSSRRGIWELLKRYQ	1020
Qy	1021	GRTIILSTHHMDEADVLDGRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL	1080
Db	1021	GRTIILSTHHMDEADILGRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL	1080
Qy	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKHVSEARLVEDI	1140
Db	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKHVSEARLVEDI	1140
Qy	1141	GHELTIVLPYEAAKEGAFVELFHEIDDRSLDLGISSYGISETTLEEIFLKVAEESGVDAE	1200
Db	1141	GHELTIVLPYEAAKEGAFVELFHEIDDRSLDLGISSYGISETTLEEIFLKVAEESGVDAE	1200
Qy	1201	TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDIPESRETDLGMDGKGSYQVK	1260
Db	1201	TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDIPESRETDLGMDGKGSYQVK	1260
Qy	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
Db	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
Qy	1321	PWMYNEQYTFVSNDAPEDTGTLELLNALTCDPGFGTRCMEGNPIPDTPCQAGEEWTAP	1380
Db	1321	PWMYNEQYTFVSNDAPEDMGTQELNALTCDPGFGTRCMEGNPIPDTPCLAGEEDWTISP	1380
Qy	1381	VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADILQDL	1440
Db	1381	VPQSIIVDLFQNGNWTMKNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADILQNL	1440
Qy	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK	1500
Db	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSHEVNDATKQMKK	1500
Qy	1501	HLKLAKDSSADRFLNSLGRFMTGLDTRNNVVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
Db	1501	LLKLTKDTSADRFLNSLGRFMAGLDTKNNVVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
Qy	1561	GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSIICVIFAMSFVPASFVFLIQR	1620
Db	1561	GENPSQYGITAFNHPLNLTQQLSEVALMTTSVDVLVSIICVIFAMSFVPASFVFLIQR	1620
Qy	1621	VSKAKHLQFISGVKPIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL	1680
Db	1621	VSKAKHLQFISGVKPIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL	1680
Qy	1681	LLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN	1740
Db	1681	LLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN	1740
Qy	1741	DILKSFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG	1800
Db	1741	DILKSFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG	1800
Qy	1801	VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Db	1801	VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Qy	1861	YRRKRKPAVDRICIGIPPGEFCGLLGUNGAGKSSTFKMLTGDTTVTRGDAFLNKNLSILSN	1920
Db	1861	YRRKRKPAVDRICIGIPPGEFCGLLGUNGAGKSSTFKMLTGDPVTRGDAFLNKNLSILSN	1920
Qy	1921	IHEVHQNMGYCQPFDAITELLTGREHVEFFALLRGVPEKEVGKFGWEAIRKGLVKYGEK	1980
Db	1921	IHEVHQNMGYCQPFDAITELLTGREHVEFFALLRGVPEKEVGKFGWEAIRKGLVKYGEK	1980
Qy	1981	YAGNYSGGNKRKLSTAMALIGPPVVFLEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	1981	YASNYSGGNKRKLSTAMALIGPPVVFLEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040

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Qy      2041 SHSMEECEALCTRMALMVNGRFRCLGSGVQHLKRNFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
          |||
Db      2041 SHSMEECEALCTRMALMVNGRFRCLGSGVQHLKRNFGDGYTIVVRIAGSNPDLKPVQEFFG 2100

Qy      2101 LAFPGSVPEKEHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFN 2160
          |||
Db      2101 LAFPGSVLKEKHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFN 2160

Qy      2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
          |||
Db      2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201

```

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477 homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758 homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.3	343	1	NOD1_RHISN	P55476 rhizobium s
10	366	3.2	304	1	NOD1_RHIS3	P72335 rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879 escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	344.5	3.0	340	1	NOD1_RHILO	P23703 rhizobium l
14	343.5	3.0	347	1	NOD1_RHIGA	P50332 rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183 homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618 rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776 escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624 escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447 mus musculu

RESULT 2

ABC1_MOUSE

```

ID  ABC1_MOUSE      STANDARD;      PRT;  2261 AA.
AC  P41233;
DT  01-FEB-1995 (Rel. 31, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE  transporter 1) (ATP-binding cassette 1) (ABC-1).
GN  ABCA1 OR ABC1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DBA/2; TISSUE=Macrophage;
RX  MEDLINE=94375008; PubMed=8088782;
RA  Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT  "Cloning of two novel ABC transporters mapping on human chromosome
RT  9.";
RL  Genomics 21:150-159(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=21251004; PubMed=11352567;
RA  Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT  "Human and mouse ABCA1 comparative sequencing and transgenesis

```

RT studies revealing novel regulatory sequences.";

RL Genomics 73:66-76(2001).

CC -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
 TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
 TRANSPORT (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
 LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.

CC -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
 EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
 ATP BINDING CASSETTE (ABC) DOMAIN.

CC -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
 similarity).

CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

DR EMBL; X75926; CAA53530.1; ALT_INIT.
 DR EMBL; AF287263; AAG39073.1; ALT_INIT.
 DR MGD; MGI:99607; Abcal.
 DR GO; GO:0008203; P:cholesterol metabolism; IDA.
 DR GO; GO:0030301; P:cholesterol transport; IDA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.

KW ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.

FT	TRANSMEM	26	42	POTENTIAL.
FT	TRANSMEM	640	656	POTENTIAL.
FT	TRANSMEM	690	706	POTENTIAL.
FT	TRANSMEM	717	733	POTENTIAL.
FT	TRANSMEM	749	765	POTENTIAL.
FT	TRANSMEM	771	787	POTENTIAL.
FT	TRANSMEM	1041	1057	POTENTIAL.
FT	TRANSMEM	1351	1367	POTENTIAL.
FT	TRANSMEM	1661	1677	POTENTIAL.
FT	TRANSMEM	1708	1724	POTENTIAL.
FT	TRANSMEM	1737	1753	POTENTIAL.
FT	TRANSMEM	1775	1791	POTENTIAL.
FT	TRANSMEM	1854	1870	POTENTIAL.
FT	NP_BIND	933	940	ATP (POTENTIAL).
FT	NP_BIND	1946	1953	ATP (POTENTIAL).
FT	MOD_RES	1042	1042	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	MOD_RES	2054	2054	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	820	820	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1144	1144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1294	1294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1453	1453	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	1499	1499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1504	1504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1637	1637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2238	2238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1567	1568	MISSING (IN REF. 2).
FT	CONFLICT	2024	2024	MISSING (IN REF. 2).
SQ	SEQUENCE	2261	AA; 254011 MW; FAE62B21FD1D09F9 CRC64;	

Query Match 95.1%; Score 10906; DB 1; Length 2261;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFS	60
Db	61	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLYSQRDT	120
Qy	61	SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH	120
Db	121	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLQXNVGLQ	180
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELGCLPREKLAARVLRNSMDILKPIL	180
Db	181	KVFLQGYQLHLASLCNGSKLEELIQLGDAEVSALCGLPRKKLDAARVLRNMDILKPVV	240
Qy	181	RTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRWSDMRQEVFMFLTNVNSSSSTQI	240
Db	241	TKLNSTSHLPTQHLAEATTVLLDSLGLAQELFSTKWSDMRQEVFMFLTNVNSSSSTQI	300
Qy	241	YQAVSRIVCGHPEGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK	300
Db	301	YQAVSRIVCGHPEGGLKIKSLNWYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK	360
Qy	301	NLESSPLSRRIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	360
Db	361	NLESSPLSRRIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	420
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTADQDIVAFLAKHPEDVQSSNGS	420
Db	421	PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTADQDIMAFLAKNPEDVQSPNGS	480
Qy	421	VYTWREAFNETNQAIQTISRMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTG	480
Db	481	VYTWREAFNETNQAIQTISRMECVNLNKLEPIPTVRLINKSMELDERKFWAGIVFTG	540
Qy	481	ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	540
Db	541	ITPDSVELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	600
Qy	541	EQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIGIV	600
Db	601	EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIISIV	660
Qy	601	YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKGNLLPYSDPSVVFV	660
Db	661	YEKEARLKETMRIMGLDNGILWFSWVSSLIPLLVSAGLLVVILKGNLLPYSDPSVVFV	720
Qy	661	FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFTLKIFAS	720
Db	721	FLSVFAMVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFSIKIFAS	780
Qy	721	LLSPVAFGFGCEYFALFEEQIGVQWDLNFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW	780
Db	781	LLSPVAFGFGCEYFALFEEQIGVQWDLNFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW	840
Qy	781	YIEAVFPGQYGI PRPWYFPCTKSYWFGEESEKSHPGSNQKRISIEICMEEEPHTHLKLGVS	840
Db	841	YIEAVFPGQYGI PRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHTHLRLGVS	900
Qy	841	IQLNVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL	900

Db 901 IQNLVKVYRDGMKVAVDGLALNFYEQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960
 Qy 901 GKDIRSEMSTIRQNLGVC PQHNVLFDMLTVEEHIWFYARLKLSEKHVKAEME QMALDVG 960
 Db 961 GKDIRSEMSSIRQNLGVC PQHNVLFDMLTVEEHIWFYARLKLSEKHVKAEME QMALDVG 1020
 Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKRYQ 1020
 Db 1021 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKRYQ 1080
 Qy 1021 GRTIILSTHHMDEADVLDGRIAII SHGKLCCVGS SFLKNQLGTGYLTLVKKDVES SLS 1080
 Db 1081 GRTIILSTHHMDEADILGRIAII SHGKLCCVGS SFLKNQLGTGYLTLVKKDVES SLS 1140
 Qy 1081 SCRNSSTVSYLKKE DSVQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
 Db 1141 SCRNSSTVSCLKKE DSVQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1200
 Qy 1141 GHELT YVLPYEA AKEGAFVELFHEIDDR LSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
 Db 1201 GHELT YVLPYEA AKEGAFVELFHEIDDR LSDLGISSYGISETTLEEIFLKVAEESGVDAE 1260
 Qy 1201 TSDGTL PARRNRRAF GDKQSC LRPFTEDDAADPNDS DIDPESRETDL LSGMDGKGSYQVK 1260
 Db 1261 TSDGTL PARRNRRAF GDKQSC LRPFTEDDAADPNDS DIDPESRETDL LSGMDGKGSYQLK 1320
 Qy 1261 GWKLTQQQFVALLWKRL LIARRSRKGFFAQIVLP AVFVCIALVFS LIVPPFGKYPSLELQ 1320
 Db 1321 GWKLTQQQFVALLWKRL LIARRSRKGFFAQIVLP AVFVCIALVFS LIVPPFGKYPSLELQ 1380
 Qy 1321 PWMYNEQYTFVSNDA PEDTGTLELLNALT KDPGFGTRCMEGNPIPDTPCQAGEEWT TAP 1380
 Db 1381 PWMYNEQYTFVSNDA PEDMGTQELLNALT KDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440
 Qy 1381 VPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPQ RKQNTADI LQDL 1440
 Db 1441 VPQSI VDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPQ RKQKTADI LQNL 1500
 Qy 1441 TGRNISDYL VKTYVQII AKSLKNKIWNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500
 Db 1501 TGRNISDYL VKTYVQII AKSLKNKIWNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560
 Qy 1501 HLKLAKDSSADRFLNS LGRFMTGLDTRNNVKVWFNNKGWHAISSFLN VINNAILRANLQK 1560
 Db 1561 LLKLT KDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLN VINNAILRANLQK 1620
 Qy 1561 GENPSHYGITAFNHPLNLT KQQLSEVAPMTTSVDVLSICVIFAMSFVPASFVFLIQR 1620
 Db 1621 GENPSQYGITAFNHPLNLT KQQLSEVALMTTSVDVLSICVIFAMSFVPASFVFLIQR 1680
 Qy 1621 VSKAKHLQFISGVKPV IYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYV SSTNL PVLAL 1680
 Db 1681 VSKAKHLQFISGVKPV IYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYV SSTNL PVLAL 1740
 Qy 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
 Db 1741 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1800
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920
 Qy 1861 YRRKRKPAVDRICVGI PPGECEG LLGVNGAGKSSTFKMLTGDTTVTRGDAFLNRNSILSN 1920
 Db 1921 YRRKRKPAVDRICIGI PPGECEG LLGVNGAGKSTTFKMLTGDTPVTRGDAFLNKNSILSN 1980
 Qy 1921 IHEVHQNMGYCQPFDAITELLTGREHVEFFALLRGVPEKEVGKVGGEWAIRKGLVKYGEK 1980

Db	1981	IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGKLVKYGEK	2040
Qy	1981	YAGNYSGGNKRKRLSTAMALIGGPPVVFLEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	2041	YASNYSGGNKRKRLSTAMALIGGPPVVFLEPTTGMDPKARRFLWNCALSIVKEGRSVVLT	2100
Qy	2041	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG	2100
Db	2101	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG	2160
Qy	2101	LAFPGSVPEKEHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF	2160
Db	2161	LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF	2220
Qy	2161	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2201
Db	2221	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2261

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NEWS	4	Feb 24	TEMA now available on STN
NEWS	5	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS	6	Feb 26	PCTFULL now contains images
NEWS	7	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
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NEWS	9	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS	10	Apr 11	Display formats in DGENE enhanced
NEWS	11	Apr 14	MEDLINE Reload
NEWS	12	Apr 17	Polymer searching in REGISTRY enhanced
NEWS	13	SEP 09	CA/CAPLUS records now contain indexing from 1907 to the present
NEWS	14	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS	15	Apr 28	RDISCLOSURE now available on STN
NEWS	16	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS	17	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS	18	May 15	Supporter information for ENCOMPAT and ENCOMPLIT updated
NEWS	19	May 19	Simultaneous left and right truncation added to WSCA
NEWS	20	May 19	RAPRA enhanced with new search field, simultaneous left and right truncation
NEWS	21	Jun 06	Simultaneous left and right truncation added to CBNB
NEWS	22	Jun 06	PASCAL enhanced with additional data
NEWS	23	Jun 20	2003 edition of the FSTA Thesaurus is now available
NEWS	24	Jun 25	HSDB has been reloaded
NEWS	25	Jul 16	Data from 1960-1976 added to RDISCLOSURE
NEWS	26	Jul 21	Identification of STN records implemented
NEWS	27	Jul 21	Polymer class term count added to REGISTRY
NEWS	28	Jul 22	INPADOC: Basic index (/BI) enhanced; Simultaneous Left and Right Truncation available
NEWS	29	AUG 05	New pricing for EUROPATFULL and PCTFULL effective August 1, 2003
NEWS	30	AUG 13	Field Availability (/FA) field enhanced in BEILSTEIN
NEWS	31	AUG 15	PATDPAFULL: one FREE connect hour, per account, in September 2003
NEWS	32	AUG 15	PCTGEN: one FREE connect hour, per account, in September 2003
NEWS	33	AUG 15	RDISCLOSURE: one FREE connect hour, per account, in September 2003
NEWS	34	AUG 15	TEMA: one FREE connect hour, per account, in September 2003
NEWS	35	AUG 18	Data available for download as a PDF in RDISCLOSURE
NEWS	36	AUG 18	Simultaneous left and right truncation added to PASCAL
NEWS	37	AUG 18	FROSTI and KOSMET enhanced with Simultaneous Left and Right

Truncation

NEWS 38 AUG 18 Simultaneous left and right truncation added to ANABSTR

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 L1 369 SCHMITZ GERD

=> s klucken jochen /au
 L2 19 KLUCKEN JOCHEN

=> s atp (p) binding (p) cassette (p) gene
 L3 3913 ATP (P) BINDING (P) CASSETTE (P) GENE

=> s abcal
 L4 1030 ABCA1

=> s atp (s) binding (s) cassette (s) gene
 L5 3077 ATP (S) BINDING (S) CASSETTE (S) GENE

=> s atp (s) binding (s) cassette (s) gene (s) protein
 L6 2046 ATP (S) BINDING (S) CASSETTE (S) GENE (S) PROTEIN

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L2 ANSWER 1 OF 19 MEDLINE on STN

ACCESSION NUMBER: 2003356553 MEDLINE
DOCUMENT NUMBER: 22745349 PubMed ID: 12861035
TITLE: High efficacy of clonal growth and expansion of adult
neural stem cells.
AUTHOR: Wachs Frank-Peter; Couillard-Despres Sebastien; Engelhardt
Maren; Wilhelm Daniel; Ploetz Sonja; Vroemen Maurice;
Kaesbauer Johanna; Uyanik Goekhan; **Klucken Jochen**
; Karl Claudia; Tebbing Johanna; Svendsen Clive; Weidner
Norbert; Kuhn Hans-Georg; Winkler Juergen; Aigner Ludwig
CORPORATE SOURCE: Volkswagen-Foundation Junior Group, University of
Regensburg, Germany.
SOURCE: LABORATORY INVESTIGATION, (2003 Jul) 83 (7) 949-62.
Journal code: 0376617. ISSN: 0023-6837.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200308
ENTRY DATE: Entered STN: 20030801
Last Updated on STN: 20030813
Entered Medline: 20030812

L2 ANSWER 2 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2003:366865 BIOSIS
DOCUMENT NUMBER: PREV200300366865
TITLE: High efficacy of clonal growth and expansion of adult
neural stem cells.
AUTHOR(S): Wachs, Frank-Peter; Couillard-Despres, Sebastien;
Engelhardt, Maren; Wilhelm, Daniel; Ploetz, Sonja; Vroemen,
Maurice; Kaesbauer, Johanna; Uyanik, Goekhan; **Klucken,**
Jochen; Karl, Claudia; Tebbing, Johanna; Svendsen,
Clive; Weidner, Norbert; Kuhn, Hans-Georg; Winkler,
Juergen; Aigner, Ludwig (1)
CORPORATE SOURCE: (1) Department of Neurology, University of Regensburg,
Franz-Josef-Strauss-Allee 11, D-93053, Regensburg, Germany:
ludwig.aigner@klinik.uni-regensburg.de Germany
SOURCE: Laboratory Investigation, (July 2003, 2003) Vol. 83, No. 7,
pp. 949-962. print.
ISSN: 0023-6837.
DOCUMENT TYPE: Article
LANGUAGE: English

L2 ANSWER 3 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2001:64994 BIOSIS
DOCUMENT NUMBER: PREV200100064994
TITLE: Genomic organization and characterization of the promoter
of the human ATP-binding cassette transporter-G1 (ABCG1)
gene.
AUTHOR(S): Langmann, Thomas; Porsch-Oezcueruemez, Mustafa; Unkelbach,
Uwe; **Klucken, Jochen**; Schmitz, Gerd (1)
CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Franz-Josef-Strauss-
Allee 11, 93042, Regensburg: gerd.schmitz@klinik.uni-
regensburg.de Germany
SOURCE: Biochimica et Biophysica Acta, (15 November, 2000) Vol.
1494, No. 1-2, pp. 175-180. print.
ISSN: 0006-3002.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 4 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2000:346957 BIOSIS
DOCUMENT NUMBER: PREV200000346957

TITLE: Identification of a novel human sterol-sensitive ATP-binding cassette transporter (ABCA7).

AUTHOR(S): Kaminski, Wolfgang E.; Orso, Evelyn; Diederich, Wendy; Klucken, Jochen; Drobnik, Wolfgang; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany

SOURCE: Biochemical and Biophysical Research Communications, (July 5, 2000) Vol. 273, No. 2, pp. 532-538. print. ISSN: 0006-291X.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 5 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2000:113448 BIOSIS

DOCUMENT NUMBER: PREV200000113448

TITLE: ABCG1 (ABC8), the human homolog of the Drosophila white gene, is a regulator of macrophage cholesterol and phospholipid transport.

AUTHOR(S): Klucken, Jochen; Buechler, Christa; Orso, Evelyn; Kaminski, Wolfgang E.; Porsch-Oezcueruemez, Mustafa; Liebisch, Gerhard; Kapinsky, Michael; Diederich, Wendy; Drobnik, Wolfgang; Dean, Michael; Allikmets, Rando; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany

SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (Jan. 18, 2000) Vol. 97, No. 2, pp. 817-822. ISSN: 0027-8424.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 6 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2000:96559 BIOSIS

DOCUMENT NUMBER: PREV200000096559

TITLE: Regulation of scavenger receptor CD163 expression in human monocytes and macrophages by pro- and antiinflammatory stimuli.

AUTHOR(S): Buechler, Christa; Ritter, Mirko; Orso, Evelyn; Langmann, Thomas; Klucken, Jochen; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institut fuer Klinische Chemie und Laboratoriumsmedizin, Klinikum der Universitaet Regensburg, Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany

SOURCE: Journal of Leukocyte Biology, (Jan., 2000) Vol. 67, No. 1, pp. 97-103. ISSN: 0741-5400.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 7 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1999:386551 BIOSIS

DOCUMENT NUMBER: PREV199900386551

TITLE: The gene encoding ATP-binding cassette transporter 1 is mutated in Tangier disease.

AUTHOR(S): Bodzioch, Marek; Orso, Evelyn; Klucken, Jochen; Langmann, Thomas; Boettcher, Alfred; Diederich, Wendy; Drobnik, Wolfgang; Barlage, Stefan; Buechler, Christa; Porsch-Oezcueruemez, Mustafa; Kaminski, Wolfgang E.;

Hahmann, Harry W.; Oette, Kurt; Rothe, Gregor; Aslanidis, Charalampos; Lackner, Karl J.; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, D-93042, Regensburg Germany

SOURCE: Nature Genetics, (Aug., 1999) Vol. 22, No. 4, pp. 347-351. ISSN: 1061-4036.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 8 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1999:247874 BIOSIS

DOCUMENT NUMBER: PREV199900247874

TITLE: Molecular cloning of the human ATP-binding cassette transporter 1 (hABC1): Evidence for sterol-dependent regulation in macrophages.

AUTHOR(S): Langmann, Thomas; **Klucken, Jochen**; Reil, Markus; Liebisch, Gerhard; Luciani, Marie-Francoise; Chimini, Giovanna; Kaminski, Wolfgang E.; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany

SOURCE: Biochemical and Biophysical Research Communications, (April 2, 1999) Vol. 257, No. 1, pp. 29-33. ISSN: 0006-291X.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 9 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1997:522758 BIOSIS

DOCUMENT NUMBER: PREV199799821961

TITLE: Scavenging, signalling and adhesion coupling in macrophages: Implications for atherogenesis.

AUTHOR(S): Schmitz, Gerd (1); Orso, Evelyn; Rothe, Gregor; **Klucken, Jochen**

CORPORATE SOURCE: (1) Inst. Clinical Chem. Lab. Med., Univ. Regensburg, Franz-Josef-Strauss-Allee 11, D-93053 Regensburg Germany

SOURCE: Current Opinion in Lipidology, (1997) Vol. 8, No. 5, pp. 287-300. ISSN: 0957-9672.

DOCUMENT TYPE: General Review

LANGUAGE: English

L2 ANSWER 10 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1997:61424 BIOSIS

DOCUMENT NUMBER: PREV199799360627

TITLE: Peripheral blood mononuclear phagocyte subpopulations as cellular markers in hypercholesterolemia.

AUTHOR(S): Rothe, Gregor; Gabriel, Holger; Kovacs, Eva; **Klucken, Jochen**; Stoehr, Josef; Kindermann, Wilfried; Schmitz, Gerd

CORPORATE SOURCE: Inst. Clinical Chemistry Lab. Med., Univ. Regensburg, Franz-Josef-Strauss-Allee 11, D-93053 Regensburg Germany

SOURCE: Arteriosclerosis Thrombosis and Vascular Biology, (1996) Vol. 16, No. 12, pp. 1437-1447. ISSN: 1079-5642.

DOCUMENT TYPE: Article

LANGUAGE: English

L2 ANSWER 11 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:9149 CAPLUS

DOCUMENT NUMBER: 135:1154

TITLE: Genomic organization and characterization of the promoter of the human ATP-binding cassette transporter-G1 (ABCG1) gene

AUTHOR(S): Langmann, Thomas; Porsch-Ozcurumez, Mustafa; Unkelbach, Uwe; Klucken, Jochen; Schmitz, Gerd

CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, 93042, Germany

SOURCE: Biochimica et Biophysica Acta (2000), 1494(1-2), 175-180
CODEN: BBACAQ; ISSN: 0006-3002

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 12 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:426543 CAPLUS

DOCUMENT NUMBER: 133:220696

TITLE: Identification of a Novel Human Sterol-Sensitive ATP-Binding Cassette Transporter (ABCA7)

AUTHOR(S): Kaminski, Wolfgang E.; Orso, Evelyn; Diederich, Wendy; Klucken, Jochen; Drobnik, Wolfgang; Schmitz, Gerd

CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, D-93042, Germany

SOURCE: Biochemical and Biophysical Research Communications (2000), 273(2), 532-538
CODEN: BBRCA9; ISSN: 0006-291X

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

L2 ANSWER 13 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:227775 CAPLUS

DOCUMENT NUMBER: 132:275181

TITLE: ATP-binding cassette genes and proteins for diagnosis and treatment of lipid disorders and inflammatory diseases

INVENTOR(S): Schmitz, Gerd; Klucken, Jochen

PATENT ASSIGNEE(S): Bayer Aktiengesellschaft, Germany

SOURCE: PCT Int. Appl., 154 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000018912	A2	20000406	WO 1999-EP6991	19990921
WO 2000018912	A3	20000817		
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

CA 2344107	AA	20000406	CA 1999-2344107	19990921
AU 9959804	A1	20000417	AU 1999-59804	19990921
EP 1115865	A2	20010718	EP 1999-969740	19990921
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002525111	T2	20020813	JP 2000-572359	19990921
PRIORITY APPLN. INFO.:			US 1998-101706P	P 19980925
			WO 1999-EP6991	W 19990921

L2 ANSWER 14 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2000:82248 CAPLUS
 DOCUMENT NUMBER: 132:248860
 TITLE: ABCG1 (ABC8), the human homolog of the Drosophila white gene, is a regulator of macrophage cholesterol and phospholipid transport
 AUTHOR(S): Klucken, Jochen; Buchler, Christa; Orso, Evelyn; Kaminski, Wolfgang E.; Porsch-Ozcurumez, Mustafa; Liebisch, Gerhard; Kapinsky, Michael; Diederich, Wendy; Drobnik, Wolfgang; Dean, Michael; Allikmets, Rando; Schmitz, Gerd
 CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, 93042, Germany
 SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(2), 817-822
 CODEN: PNASA6; ISSN: 0027-8424
 PUBLISHER: National Academy of Sciences
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2000:62019 CAPLUS
 DOCUMENT NUMBER: 132:206903
 TITLE: Regulation of scavenger receptor CD163 expression in human monocytes and macrophages by pro- and antiinflammatory stimuli
 AUTHOR(S): Buechler, Christa; Ritter, Mirko; Orso, Evelyn; Langmann, Thomas; Klucken, Jochen; Schmitz, Gerd
 CORPORATE SOURCE: Institut fur Klinische Chemie und Laboratoriumsmedizin, Klinikum der Universitat Regensburg, Regensburg, D-93042, Germany
 SOURCE: Journal of Leukocyte Biology (2000), 67(1), 97-103
 CODEN: JLBIE7; ISSN: 0741-5400
 PUBLISHER: Federation of American Societies for Experimental Biology
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1999:500267 CAPLUS
 DOCUMENT NUMBER: 131:255941
 TITLE: The gene encoding ATP-binding cassette transporter 1 is mutated in Tangier disease
 AUTHOR(S): Bodzioch, Marek; Orso, Evelyn; Klucken, Jochen; Langmann, Thomas; Bottcher, Alfred; Diederich, Wendy; Drobnik, Wolfgang; Barlage, Stefan; Buchler, Christa; Porsch-Ozcurumez, Mustafa; Kaminski, Wolfgang E.; Hahmann, Harry W.; Oette, Kurt; Rothe, Gregor; Aslanidis, Charalampos; Lackner, Karl J.; Schmitz,

CORPORATE SOURCE: Gerd
Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg,
D-93042, Germany
SOURCE: Nature Genetics (1999), 22(4), 347-351
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature America
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS
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L2 ANSWER 17 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1999:199124 CAPLUS
DOCUMENT NUMBER: 131:83698
TITLE: Molecular cloning of the human ATP-binding cassette
transporter 1 (hABC1): evidence for sterol-dependent
regulation in macrophages
AUTHOR(S): Langmann, Thomas; **Klucken, Jochen**; Reil,
Markus; Liebisch, Gerhard; Luciani, Marie-Francoise;
Chimini, Giovanna; Kaminski, Wolfgang E.; Schmitz,
Gerd
CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg, 93042,
Germany
SOURCE: Biochemical and Biophysical Research Communications
(1999), 257(1), 29-33
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
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L2 ANSWER 18 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1997:675284 CAPLUS
DOCUMENT NUMBER: 127:344497
TITLE: Scavenging, signaling and adhesion coupling in
macrophages: implications for atherogenesis
AUTHOR(S): Schmitz, Gerd; Orso, Evelyn; Rothe, Gregor;
Klucken, Jochen
CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg,
D-93053, Germany
SOURCE: Current Opinion in Lipidology (1997), 8(5), 287-300
CODEN: COPLEU; ISSN: 0957-9672
PUBLISHER: Rapid Science Publishers
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

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ACCESSION NUMBER: 1997:54357 CAPLUS
DOCUMENT NUMBER: 126:116448
TITLE: Peripheral blood mononuclear phagocyte subpopulations
as cellular markers in hypercholesterolemia
AUTHOR(S): Rothe, Gregor; Gabriel, Holger; Kovacs, Eva;
Klucken, Jochen; Stoehr, Josef; Kindermann,
Wilfried; Schmitz, Gerd
CORPORATE SOURCE: Inst. Clinical Chem. & Lab. Medicine, Univ.
Regensburg, Germany
SOURCE: Arteriosclerosis, Thrombosis, and Vascular Biology
(1996), 16(12), 1437-1447
CODEN: ATVBFA; ISSN: 1079-5642
PUBLISHER: American Heart Association

DOCUMENT TYPE:
LANGUAGE:

Journal
English